

SEQUENCE LISTING

Sub A

<110> Dattwyler, Raymond J.
 Seinost, Gerald
 Dykhuizen, Daniel
 Luft, Benjamin J.
 Maria J.C. Gomes-Solecki

<120> Groups of *Borrelia burgdorferi* and
Borrelia afzelii That Cause Lyme Disease in Humans

<130> 2631.1002-001

<150> US 60/140,042
<151> 1999-06-18

<160> 84

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<220>
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<210> 5
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Sub A1

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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys
 100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
 115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
 145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtc cat gga tcc 573
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 180 185 190

<210> 6
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<212> PRT
<213> borrelia burgdorferi

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Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu 45
35 40
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys 60
50 55
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu 80
65 70 75
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys 95
85 90
Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys Lys 110
100 105
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu 125
115 120
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys 140
130 135
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu 160
145 150 155
Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 175
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Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Ser 190
180 185

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1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

SubRAI

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr 35 40 45	144
tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys 50 55 60	192
ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu 65 70 75 80	240
tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn 85 90 95	288
gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln 100 105 110	336
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu 115 120 125	384
ggg ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys 130 135 140	432
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe 145 150 155 160	480
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn 165 170 175	528
gct gtt aaa gag ctt aca agt cct att gt Ala Val Lys Glu Leu Thr Ser Pro Ile 180 185	557

<210> 8
<211> 184
<212> PRT
<213> *Borrelia burgdorferi*

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Sub A'

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Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys
100 105 110
Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly
115 120 125
Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys
130 135 140
His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys
145 150 155 160
Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala
165 170 175
Val Lys Glu Leu Thr Ser Pro Ile
180

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<210> 9
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<212> DNA
<213> Borrelia burgdorferi

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<221> CDS
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aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30

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aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144
Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala
35 40 45

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gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att gct gct 192
Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala
50 55 60

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aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat acc gaa 240
Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu
65 70 75 80

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aat aat cac aat gga tca ttg tta gcg gga gct tat gca ata tca acc 288
Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
85 90 95

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cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta aag gaa 336
Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu
100 105 110

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aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat aaa tta 384
Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu
115 120 125

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aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat gct gat 432
Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp
130 135 140

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Sub A' 1

gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa ggt gct	480
Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala	
145 150 155 160	
gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca aaa gca	528
Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala	
165 170 175	
gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct gtt	576
Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val	
180 185 190	
gtg	579
Val	

<210> 10
<211> 192
<212> PRT
<213> Borrelia burgdorferi

<400> 10	
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20 25 30	
Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val	
35 40 45	
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys	
50 55 60	
Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn	
65 70 75 80	
Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu	
85 90 95	
Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys	
100 105 110	
Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys	
115 120 125	
Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala	
130 135 140	
Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu	
145 150 155 160	
Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala	
165 170 175	
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180 185 190	

<210> 11
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<212> DNA
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aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu 20 25 30	96	
aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala 35 40 45	144	
gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt gct aaa Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys 50 55 60	192	
gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat gaa gca Ala Ile Gly Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala 65 70 75 80	240	
aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca acc tta Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu 85 90 95	288	
ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta aag gaa Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu 100 105 110	336	
aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act aaa cta Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu 115 120 125	384	
aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat gaa aat Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn 130 135 140	432	
gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat aag ggc Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Gly Lys Asp Lys Gly 145 150 155 160	480	
gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta tca aaa Val Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys 165 170 175	528	
gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro 180 185 190	576	
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<213> Borrelia brgdorferi		

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 35 40 45
 Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala
 50 55 60
 Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn
 65 70 75 80
 Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile
 85 90 95
 Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys
 100 105 110
 Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys
 115 120 125
 Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala
 130 135 140
 Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val
 145 150 155 160
 Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala
 165 170 175
 Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val
 180 185 190

<210> 13
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<213> *Borrelia burgdorferi*

<220>
<221> CDS
<222> (1)...(576)

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aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
35 40 45

gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc 192
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
50 55 60

aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc aat cag 240
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln
65 70 75 80

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Sub A1

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85 90 95	
ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys	336
100 105 110	
att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys	384
115 120 125	
agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala	432
130 135 140	
caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca Gln Arg Ala Ile Leu Lys His Ala Asn Lys Asp Lys Gly Ala Ala	480
145 150 155 160	
gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala	528
165 170 175	
caa gac aca tta aaa aat gct ggt aaa gag ctt aca agt cct att gtg Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val	576
180 185 190	

<210> 14
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<212> PRT
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Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val	
35 40 45	
Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys	
50 55 60	
Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser	
65 70 75 80	
Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile	
85 90 95	
Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile	
100 105 110	
Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser	
115 120 125	
Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln	
130 135 140	
Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu	
145 150 155 160	
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln	
165 170 175	

Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
 180 185 190

<210> 15
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 aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45

gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc 192
 Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
 50 55 60

aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag 240
 Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln
 65 70 75 80

agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta 288
 Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu
 85 90 95

ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag 336
 Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys
 100 105 110

att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa 384
 Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys
 115 120 125

agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca 432
 Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala
 130 135 140

caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca 480
 Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
 145 150 155 160

gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528
 Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
 165 170 175

Sust AI

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576
 Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
 180 185 190

<210> 16
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<400> 16
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 20 25 30
 Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val 45
 35 40 45
 Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys 60
 50 55 60
 Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser 80
 65 70 75 80
 Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile 95
 85 90 95
 Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile 110
 100 105 110
 Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser 125
 115 120 125
 Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln 140
 130 135 140
 Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu 160
 145 150 155 160
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln 175
 165 170 175
 Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val 190
 180 185

<210> 17
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<220>
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 <222> (1)...(573)

<400> 17
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 aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30
 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc 144
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45

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Sub A1

gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa 192
Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys
50 55 60

gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca 240
Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala
65 70 75 80

gat cac aac gga tca tta ata tca gga gca tat tta att tca aac tta 288
Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu
85 90 95

ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca 336
Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala
100 105 110

gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta 384
Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu
115 120 125

aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat 432
Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn
130 135 140

gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc gct 480
Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala
145 150 155 160

gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca 528
Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala
165 170 175

gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc cct 573
Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro
180 185 190

<210> 18
<211> 190
<212> PRT
<213> *Borrelia burgdorferi*

<400> 18
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
1 5 10 15
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
20 25 30
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
35 40 45
Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala
50 55 60
Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp
65 70 75 80
His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile
85 90 95
Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu
100 105 110

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SuAI
Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys
115 120 125
Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala
130 135 140
Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp
145 150 155 160
Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala
165 170 175
Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro
180 185 190

<210> 19
<211> 553
<212> DNA
<213> *Borrelia burgdorferi*

<220>
<221> CDS
<222> (1)...(553)

<400> 19
atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg 48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
1 5 10 15
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct 144
Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
35 40 45
gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act 192
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
50 55 60
aaa gct att ggt aaa aaa ata gat aac aat gct ggt ttg ggt gct gaa 240
Lys Ala Ile Gly Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu
65 70 75 80
gtg ggt caa aac gga tca ttg cta gca gga gct tat gca atc tca act 288
Val Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
85 90 95
gta ata ata gaa aaa ttg agc aca tta aaa aat gta gaa gaa tta aaa 336
Val Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys
100 105 110
gaa aaa att aca aag gct aag gat tgt tct gaa aaa ttc act aaa aaa 384
Glu Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys
115 120 125
tta aaa gat agc cgc gca gag ctt ggt aaa aaa gat gcc agt gat gat 432
Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp
130 135 140

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gat gca aaa aaa gct att tta aaa aca aat caa gct aac gat aag ggt 480
Asp Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly
145 150 155 160

gct aaa gaa ctt aaa gag tta ttt gaa gca gta gaa agc ttg tca aaa 528
Ala Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys
165 170 175

gcg gct aaa gag atg cta aac aag t 553
Ala Ala Lys Glu Met Leu Asn Lys
180

<210> 20
<211> 183
<212> PRT
<213> Borrelia burgdorferi

<400> 20
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
1 5 10 15
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
20 25 30
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
35 40 45
Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
50 55 60
Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu Val
65 70 75 80
Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Val
85 90 95
Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys Glu
100 105 110
Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys Leu
115 120 125
Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp Asp
130 135 140
Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly Ala
145 150 155 160
Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys Ala
165 170 175
Ala Lys Glu Met Leu Asn Lys
180

<210> 21
<211> 582
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(582)

<400> 21 48
atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
1 5 10 15

Sufu AI

aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu 20 25 30	96
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala 35 40 45	144
gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr 50 55 60	192
aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa Lys Ala Ile Gly Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu 65 70 75 80	240
gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca aaa Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys 85 90 95	288
cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys 100 105 110	336
gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys 115 120 125	384
cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat gag Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu 130 135 140	432
aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag ggc Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly 145 150 155 160	480
gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys 165 170 175	528
gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agt cct Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro 180 185 190	576
att gtg Ile Val	582

<210> 22
<211> 193
<212> PRT
<213> *Borrelia burgdorferi*

<400> 22
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
1 5 10 15
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
20 25 30

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SubAI 1
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
35 40 45
Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
50 55 60
Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala
65 70 75 80
Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu
85 90 95
Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu
100 105 110
Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu
115 120 125
Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn
130 135 140
Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala
145 150 155 160
Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala
165 170 175
Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Ile
180 185 190
Val

<210> 23
<211> 1128
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1128)

<400> 23
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65 70 75 80

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Sukra 1

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu 85 90 95	288
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 100 105 110	336
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp 115 120 125	384
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu 130 135 140	432
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 145 150 155 160	480
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala 180 185 190	576
atg gta aat aat tca ggg aaa gat ggg aat aca tct gca aat tct gct Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala 195 200 205	624
gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile 210 215 220	672
aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu 225 230 235 240	720
ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata aaa Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys 245 250 255	768
aac gat gtt agt tta gat aat gag gca gat cac aac gga tca tta ata Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile 260 265 270	816
tca gga gca tat tta att tca aac tta ata aca aaa aaa ata agt gca Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala 275 280 285	864
ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct aag aaa Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys 290 295 300	912
tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca gat ctt Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu 305 310 315 320	960

Sub A

ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att tta aaa Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys 325 330 335	1008
aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag tta ttt Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe 340 345 350	1056
gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt act aat Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn 355 360 365	1104
tca gtt aaa gag ctt aca agc taa Ser Val Lys Glu Leu Thr Ser * 370 375	1128

<210> 24
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 24 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala 1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile 20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu 35 40 45
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile 50 55 60
His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu 65 70 75 80
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp 85 90 95
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys 100 105 110
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu 115 120 125
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys 130 135 140
Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe 145 150 155 160
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn 165 170 175
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala Met 180 185 190
Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp 195 200 205
Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr 210 215 220
Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu 225 230 235 240
Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn 245 250 255

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Sub A

Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser
260 265 270
Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile
275 280 285
Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys
290 295 300
Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly
305 310 315 320
Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr
325 330 335
Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu
340 345 350
Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser
355 360 365
Val Lys Glu Leu Thr Ser
370

<210> 25
<211> 1124
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1124)

<400> 25
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
5 10 15
1

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Ile Thr Glu Ile Ser Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110

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Sulf A1

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa ctt gga aaa tta 480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Leu Gly Lys Leu
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175.

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
180 185 190

atg gta aat aat tca gga aaa gat ggg aat aca tct gca aat tct gct 624
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
195 200 205

gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att 672
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
210 215 220

aca gaa tct aac gca gtt ctg gct gtg aaa gaa att gaa act ttg 720
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu
225 230 235 240

ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa aaa ata 768
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
245 250 255

caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg 816
Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu
260 265 270

tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa tta gat 864
Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp
275 280 285

gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat gct aag 912
Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Ile Glu Asn Ala Lys
290 295 300

aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat gcg caa 960
Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln
305 310 315 320

ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct att tta 1008
Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
325 330 335

ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa aag cta 1056
Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
340 345 350

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Sub A1
ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg ctt gct 1104
Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala
355 360 365

aat tca gtt aaa gag ctt ac 1124
Asn Ser Val Lys Glu Leu
370

<210> 26
<211> 373
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 26
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
85 90 95
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
100 105 110
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
115 120 125
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
130 135 140
Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
145 150 155 160
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
165 170 175
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala Met
180 185 190
Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp
195 200 205
Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr
210 215 220
Glu Ser Asn Ala Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu
225 230 235 240
Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln
245 250 255
Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu
260 265 270
Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly
275 280 285
Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys
290 295 300
Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu
305 310 315 320

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Gly	Ile	Glu	Asn	Val	Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile
										325	330				335
Thr	Asp	Ala	Ala	Ala	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu
										340	345				350
Lys	Ala	Val	Glu	Asn	Leu	Ala	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn
										355	360				365
Ser	Val	Lys	Glu	Leu											
										370					

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<210> 27  
<211> 1137  
<212> DNA  
<213> Artificial Sequence
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<220>
<223> OspC Chimera

<221> CDS
<222> (1) . . . (1137)

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<400> 27
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1           5                   10                  15

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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140

Sub A1
 aca gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 576
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
 180 185 190
 aaa cct tcc atg gta aat aat tca ggg aaa gat ggg aat aca tct gca 624
 Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
 195 200 205
 aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt 672
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
 210 215 220
 aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt 720
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
 225 230 235 240
 gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa 768
 Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys
 245 250 255
 aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga 816
 Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly
 260 265 270
 tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa 864
 Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys
 275 280 285
 ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag 912
 Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys
 290 295 300
 gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac 960
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His
 305 310 315 320
 aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc 1008
 Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
 325 330 335
 att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa 1056
 Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
 340 345 350
 aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg 1104
 Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
 355 360 365
 ctt act aat tca gtt aaa gag ctt aca agc taa 1137
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser *
 370 375

<210> 28
 <211> 378
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> OspC Chimera

 <400> 28
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 1 5 10 15
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
 20 25 30
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65 70 75 80
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
 180 185 190
 Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
 195 200 205
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
 210 215 220
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
 225 230 235 240
 Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys
 245 250 255
 Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly
 260 265 270
 Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys
 275 280 285
 Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys
 290 295 300
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His
 305 310 315 320
 Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
 325 330 335
 Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
 340 345 350
 Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
 355 360 365
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 370 375

Sub-A1

<210> 29
<211> 1133
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS

<222> (1) ... (1133)

<400> 29
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1 5 10 15

gct gat gag tct aat gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80

ttg tta gcg gga gct tat goa ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175

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Sub A1

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys 180 185 190	576
aaa cct tcc atg gta aat aat tca gga aaa gat ggg aat aca tct gca Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala 195 200 205	624
aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser 210 215 220	672
aaa aaa att aca gaa tct aac gca gtt ctg gct gtg aaa gaa att Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile 225 230 235 240	720
gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly 245 250 255	768
aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn 260 265 270	816
gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln 275 280 285	864
aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu 290 295 300	912
aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu 305 310 315 320	960
cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys 325 330 335	1008
gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu 340 345 350	1056
gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu 355 360 365	1104
atg ctt gct aat tca gtt aaa gag ctt ac Met Leu Ala Asn Ser Val Lys Glu Leu 370 375	1133

<210> 30

<211> 377

<212> PRT

<213> Artificial Sequence

Sub A1

<220> 30
<223> OspC Chimera

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
 20 25 30
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65 70 75 80
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
 180 185 190
 Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
 195 200 205
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
 210 215 220
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile
 225 230 235 240
 Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
 245 250 255
 Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn
 260 265 270
 Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln
 275 280 285
 Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu
 290 295 300
 Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu
 305 310 315 320
 His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys
 325 330 335
 Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
 340 345 350
 Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu
 355 360 365
 Met Leu Ala Asn Ser Val Lys Glu Leu
 370 375

<210> 31
 <211> 1112
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1112)

<400> 31 48
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65 70 75 80
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85 90 95
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
100 105 110
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115 120 125
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Leu Glu Lys
145 150 155 160
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
165 170 175
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
180 185 190
tca aga aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt 624
Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val
195 200 205

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Subsp 1

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn 210 215 220	672
gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile 225 230 235 240	720
gat gaa ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly 245 250 255	768
tta gag gcc aat tag agt aaa aac aca tca ttg tta tca gga gct tat Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr 260 265 270	816
gca ata tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu 275 280 285	864
gaa tta aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe 290 295 300	912
act aat aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu 305 310 315 320	960
act gat gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys 325 330 335	1008
gat aag ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn 340 345 350	1056
tta tca aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu 355 360 365	1104
aca agt cc Thr Ser 370	1112

<210> 32
<211> 369
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 32
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30

Sub A1
 1
 Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
 35 40 45
 Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
 50 55 60
 Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
 65 70 75 80
 Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
 85 90 95
 Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
 115 120 125
 Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
 130 135 140
 Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
 145 150 155 160
 Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
 180 185 190
 Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys
 195 200 205
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 210 215 220
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp
 225 230 235 240
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu
 245 250 255
 Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala
 260 265 270
 Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu
 275 280 285
 Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr
 290 295 300
 Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr
 305 310 315 320
 Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp
 325 330 335
 Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu
 340 345 350
 Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr
 355 360 365
 Ser

<210> 33
 <211> 1113
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1113)

<400> 33

Sub A1

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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 20 25 30	96
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 35 40 45	144
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile 50 55 60	192
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 65 70 75 80	240
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser 85 90 95	288
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys 100 105 110	336
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln 115 120 125	384
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu 130 135 140	432
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Leu Glu Lys 145 150 155 160	480
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu 165 170 175	528
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn 180 185 190	576
tca ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt . Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val 195 200 205	624
aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn 210 215 220	672
gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile 225 230 235 240	720

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Sub A1

gat gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt	768
Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser	
245 250 255	
tta gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat	816
Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr	
260 265 270	
tta att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca	864
Leu Ile Ser Asn Ile Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser	
275 280 285	
gga gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa	912
Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu	
290 295 300	
ttt act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc	960
Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly	
305 310 315 320	
gtt act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat	1008
Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp	
325 330 335	
aaa act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa	1056
Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys	
340 345 350	
aac ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag	1104
Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu	
355 360 365	
ctt aca agc	1113
Leu Thr Ser	
370	

<210> 34
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 34
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
50 55 60
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
65 70 75 80
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
85 90 95

Sub A1

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Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
100          105          110
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
115          120          125
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
130          135          140
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
145          150          155          160
Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165          170          175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
180          185          190
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
195          200          205
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
210          215          220
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp
225          230          235          240
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu
245          250          255
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu
260          265          270
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly
275          280          285
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
290          295          300
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
305          310          315          320
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
325          330          335
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
340          345          350
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
355          360          365
Thr Ser
370

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<210> 35
<211> 1112
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1112)

<400> 35
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

48

96

Sub-A1

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	144
35 40 45	
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile	192
50 55 60	
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	240
65 70 75 80	
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser	288
85 90 95	
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys	336
100 105 110	
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln	384
115 120 125	
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu	432
130 135 140	
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys	480
145 150 155 160	
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu	528
165 170 175	
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn	576
180 185 190	
tca gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val	624
195 200 205	
aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn	672
210 215 220	
gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile	720
225 230 235 240	
gat gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly	768
245 250 255	
ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala	816
260 265 270	

SulAI

tat aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn 275 280 285	864
tca gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu 290 295 300	912
gat ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu 305 310 315 320	960
aat gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala 325 330 335	1008
gct aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val 340 345 350	1056
gaa aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys 355 360 365	1104
gag ctt ac Glu Leu 370	1112
<210> 36	
<211> 369	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> OspC Chimera	
<400> 36	
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala 1 5 10 15	
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile 20 25 30	
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu 35 40 45	
Ile Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys 50 55 60	
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu 65 70 75 80	
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys 85 90 95	
Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys 100 105 110	
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu 115 120 125	
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys 130 135 140	
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu 145 150 155 160	

36/102

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<210> 37
<211> 1106
<212> DNA
<213> Artificial Sequence
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<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1106)

<400> 37
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45

```
tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
      50          55          60
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Sub A1

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu 65 70 75 80	240
tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn 85 90 95	288
gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa Val Leu Lys Asn Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln 100 105 110	336
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu 115 120 125	384
ggc ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys 130 135 140	432
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe 145 150 155 160	480
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn 165 170 175	528
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca aga Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg 180 185 190	576
aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly 195 200 205	624
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt Pro Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val 210 215 220	672
gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu 225 230 235 240	720
ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu 245 250 255	768
gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile 260 265 270	816
tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu 275 280 285	864
aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn 290 295 300	912

SulfAI

aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp 305 310 315 320	960
gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag Asp Asn Ala Gln Arg Ala Ile Leu Lys His Ala Asn Lys Asp Lys 325 330 335	1008
ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser 340 345 350	1056
aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser 355 360 365	1104

1106

cc

<210> 38
<211> 368
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 38	
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser	
1 5 10 15	
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr	
35 40 45	
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys	
50 55 60	
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu	
65 70 75 80	
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn	
85 90 95	
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln	
100 105 110	
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu	
115 120 125	
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe	
145 150 155 160	
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn	
165 170 175	
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg	
180 185 190	
Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly	
195 200 205	
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val	
210 215 220	
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu	
225 230 235 240	

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Sub A1
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu
245 250 255
Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile
260 265 270
Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu
275 280 285
Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn
290 295 300
Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp
305 310 315 320
Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys
325 330 335
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser
340 345 350
Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
355 360 365

<210> 39

<211> 1107

<212> DNA

<213> Artificial Sequence

<220>

<223> OspC Chimera

<221> CDS

<222> (1)...(1107)

<400> 39

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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
50 55 60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
65 70 75 80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
85 90 95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
100 105 110

tgc tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
 115 120 125

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
 130 135 140

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 145 150 155 160

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
 165 170 175

gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca ggg 576
 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly
 180 185 190

aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg 624
 Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
 195 200 205

cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt 672
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
 210 215 220

gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag 720
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu
 225 230 235 240

ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat 768
 Leu Ala Lys Ala Ile Gly Lys Ile Lys Asn Asp Val Ser Leu Asp
 245 250 255

aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta att 816
 Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile
 260 265 270

tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa 864
 Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu
 275 280 285

ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act 912
 Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
 290 295 300

gct aaa tta aaa ggt gaa cac aca gat ctt gct aaa gaa ggc gtt act 960
 Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr
 305 310 315 320

gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act 1008
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr
 325 330 335

aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg 1056
 Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu
 340 345 350

Sub A1

tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca 1104
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
 355 360 365

1107

agc
 Ser

<210> 40
 <211> 368
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 40
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser Ala 15
 1 5 10 15
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile 30
 20 25 30
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu 45
 35 40 45
 Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile 60
 50 55 60
 Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu 80
 65 70 75 80
 Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val 95
 85 90 95
 Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys 110
 100 105 110
 Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly 125
 115 120 125
 Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys 140
 130 135 140
 His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys 160
 145 150 155 160
 Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala 175
 165 170 175
 Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly Lys 190
 180 185 190
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 205
 195 200 205
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val 220
 210 215 220
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu 240
 225 230 235 240
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn 255
 245 250 255
 Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser 270
 260 265 270
 Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu 285
 275 280 285
 Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala 300
 290 295 300
 Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 320
 305 310 315

SubAI

Asp Asn Ala Lys Lys Ala Ile Leu Lys	Thr Asn Asn Asp Lys Thr Lys
325	330 335
Gly Ala Asp Glu Leu Glu Lys Leu Phe	Glu Ser Val Lys Asn Leu Ser
340	345 350
Lys Ala Ala Lys Glu Met Leu Thr	Asn Ser Val Lys Glu Leu Thr Ser
355	360 365

<210> 41
<211> 1106
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1106)

<400> 41	48
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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser	
1 5 10 15	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc	144
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr	
35 40 45	
tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa	192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys	
50 55 60	
ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg	240
Ile Gly Asn Asn Gly Leu Ala Asn Gln Ser Lys Asn Thr Ser Leu	
65 70 75 80	
tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat	288
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn	
85 90 95	
gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa	336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln	
100 105 110	
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt	384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu	
115 120 125	
ggc ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	

Sub A1

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe 145 150 155 160	480
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn 165 170 175	528
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca gga Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly 180 185 190	576
aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly 195 200 205	624
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val 210 215 220	672
gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu 225 230 235 240	720
ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu 245 250 255	768
gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr 260 265 270	816
ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu 275 280 285	864
aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe 290 295 300	912
act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val 305 310 315 320	960
act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys 325 330 335	1008
gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn 340 345 350	1056
ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu 355 360 365	1104
ac	1106

<211> 367
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> OspC Chimera

 <400> 42
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser Ala
 5 10 15
 1 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 20 25 30
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu
 35 40 45
 Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
 50 55 60
 Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu
 65 70 75 80
 Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val
 85 90 95
 Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys
 100 105 110
 Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly
 115 120 125
 Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys
 130 135 140
 His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys
 145 150 155 160
 Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala
 165 170 175
 Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly Lys
 180 185 190
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 195 200 205
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 210 215 220
 Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 225 230 235 240
 Ala Thr Lys Ala Ile Gly Lys Ile Gln Gln Asn Gly Gly Leu Ala
 245 250 255
 Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile
 260 265 270
 Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys
 275 280 285
 Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr
 290 295 300 320
 Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr
 305 310 315
 Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp
 325 330 335
 Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu
 340 345 350
 Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
 355 360 365

<210> 43
 <211> 633
 <212> DNA

Sub A1

<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(633)

<400> 43	48
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt	
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe	
1 5 10 15	
ata tct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct	96
Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
20 25 30	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa	144
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys	
35 40 45	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	192
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
50 55 60	
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa	240
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	
65 70 75 80	
ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca	288
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser	
85 90 95	
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta	336
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
100 105 110	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	384
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
115 120 125	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	432
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
130 135 140	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	480
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
145 150 155 160	
aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	528
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
165 170 175	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	576
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
180 185 190	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt coa aaa	624
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys	
195 200 205	

633

aaa cct taa
Lys Pro *
210

<210> 44
<211> 209
<212> PRT
<213> Borrelia burgdorferi

<400> 44
Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile
1 5 10 15
Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
20 25 30
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys Ile
35 40 45
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
50 55 60
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
65 70 75 80
His Gln Asn Asn Gly Ieu Asp Thr Glu Asn Asn His Asn Gly Ser Leu
85 90 95
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
100 105 110
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
115 120 125
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
130 135 140
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
145 150 155 160
Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
165 170 175
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
180 185 190
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys
195 200 205
Pro

<210> 45
<211> 580
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(580)

<400> 45
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15 48
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30 96

Sub A1

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	144
35 40 45	
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	192
50 55 60	
ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser	240
65 70 75 80	
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	288
85 90 95	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	336
100 105 110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	384
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gaa gcc att tta Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	432
130 135 140	
aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	480
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	528
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca tcc Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser	576
180 185 190	
atg g Met	580

<210> 46
<211> 192
<212> PRT
<213> Borrelia burgdorferi

<400> 46
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys Ile
20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60

Jack A'

His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Asn	Asn	His	Asn	Gly	Ser	Leu
65				70				75			80				
Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp
		85						90			95				
Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys
	100					105				110					
Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu
	115					120				125					
Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys
	130				135				140						
Ala	Asn	Gly	Thr	Lys	Thr	Lys	Gly	Ala	Glu	Leu	Gly	Lys	Leu	Phe	
145					150				155			160			
Glu	Ser	Val	Glu	Val	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn
							165		170			175			
Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Ser	Met
								180		185		190			

<210> 47

<211> 639

<212> DNA

<213> Borrelia garinii

<220>

<221> CDS

<222> (1)...(639)

<400> 47

atg	aaa	aag	aat	aca	tta	agt	gcg	ata	tta	atg	act	tta	ttt	tta	ttt
Met															
1					5					10					48
Lys	Lys	Asn	Thr	Leu	Ser	Ala	Ile	Leu	Met	Thr	Leu	Phe	Leu	Phe	

ata	tct	tgt	agt	aat	tca	ggg	aaa	ggg	gat	tct	gca	tct	act	aat	
Ile	Ser	Cys	Ser	Asn	Ser	Gly	Lys	Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn
20							25					30			96

cct	gct	gac	gag	tct	gcg	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agc	aaa
Pro	Ala	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys
35							40				45				144

aaa	att	aca	gat	tct	aat	gca	ttt	gta	ctt	gct	gtt	aaa	gaa	gtt	gag
Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	Val	Leu	Ala	Val	Lys	Glu	Val	Glu
50							55			60					192

act	ttg	gtt	tta	tct	ata	gat	gaa	ctt	gct	aag	aaa	gct	att	gg	caa
Thr	Leu	Val	Leu	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Lys	Ala	Ile	Gly	Gln
65					70				75			80			240

aaa	ata	gac	aat	aat	aat	ggt	tta	gct	gct	tta	aat	aat	cag	aat	gga
Lys	Ile	Asp	Asn	Asn	Gly	Leu	Ala	Ala	Leu	Asn	Asn	Gln	Asn	Gly	
85							90				95				288

tcg	ttg	tta	gca	gga	gcc	tat	gca	ata	tca	acc	cta	ata	aca	gaa	aaa
Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Thr	Glu	Lys
100							105				110				336

ttg	agt	aaa	ttg	aaa	aat	tta	gaa	gaa	tta	aag	aca	gaa	att	gca	aag
Leu	Ser	Lys	Leu	Lys	Asn	Leu	Glu	Glu	Leu	Lys	Thr	Glu	Ile	Ala	Lys
115							120				125				384

Sub A1

gct aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His 130 135 140	432
gca gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala 145 150 155 160	480
att tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys 165 170 175	528
gat tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala 180 185 190	576
cta act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser 195 200 205	624
cca aaa aaa cct taa Pro Lys Lys Pro * 210	639

<210> 48
<211> 211
<212> PRT
<213> Borrelia garinii

<400> 48

Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile 1 5 10 15
Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro 20 25 30
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 35 40 45
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr 50 55 60
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys 65 70 75 80
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser 85 90 95
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu 100 105 110
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala 115 120 125
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala 130 135 140
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile 145 150 155 160
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp 165 170 175
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu 180 185 190
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro 195 200 205

SarkAI

Lys Lys Pro
210

<210> 49
<211> 624
<212> DNA
<213> *Borrelia afzelii*

<220>
<221> CDS
<222> (1)...(624)

<400> 49

atg	aaa	aag	aat	aca	tta	agt	gcg	ata	tta	atg	act	tta	ttt	tta	ttt	48
Met	Lys	Lys	Asn	Thr	Leu	Ser	Ala	Ile	Leu	Met	Thr	Leu	Phe	Leu	Phe	
1				5				10					15			

ata	tct	tgt	aat	aat	tca	ggg	gat	tct	gca	tct	act	aat	cct	gat	96
Ile	Ser	Cys	Asn	Asn	Ser	Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	Asp
					20			25				30			

gag	tct	gca	aaa	gga	cct	aat	ctt	acc	gta	ata	agc	aaa	aaa	att	aca	144
Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Val	Ile	Ser	Lys	Lys	Ile	Thr	
					35			40				45				

gat	tct	aat	gca	ttt	tta	ctg	gct	gtg	aaa	gaa	gtt	gag	gct	ttg	ctt	192
Asp	Ser	Asn	Ala	Phe	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	
					50		55			60						

tca	tct	ata	gat	gaa	ctt	tct	aaa	gct	att	ggt	aaa	aaa	ata	aaa	aat	240
Ser	Ser	Ile	Asp	Glu	Leu	Ser	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	
					65		70			75			80			

gat	ggt	act	tta	gat	aac	gaa	gca	aat	cga	aac	gaa	tca	ttg	ata	gca	288
Asp	Gly	Thr	Leu	Asp	Asn	Glu	Ala	Asn	Arg	Asn	Glu	Ser	Leu	Ile	Ala	
					85		90			95						

gga	gct	tat	gaa	ata	tca	aaa	cta	ata	aca	caa	aaa	tta	agt	gta	ttg	336
Gly	Ala	Tyr	Glu	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Ser	Val	Leu	
					100		105					110				

aat	tca	gaa	gaa	tta	aag	aaa	aaa	att	aaa	gag	gct	aag	gat	tgt	tcc	384
Asn	Ser	Glu	Glu	Leu	Lys	Lys	Ile	Lys	Glu	Ala	Lys	Asp	Cys	Ser		
					115		120			125						

caa	aaa	ttt	act	act	aag	cta	aaa	gat	agt	cat	gca	gag	ctt	ggg	ata	432
Gln	Lys	Phe	Thr	Thr	Lys	Leu	Lys	Asp	Ser	His	Ala	Glu	Leu	Gly	Ile	
					130		135			140						

caa	agc	gtt	cag	gat	aat	gca	aaa	aaa	gct	att	tta	aaa	aca	cat	480	
Gln	Ser	Val	Gln	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	His	
					145		150			155			160			

gga	act	aaa	gac	aag	ggt	gct	aaa	gaa	ctt	gaa	gag	tta	ttt	aaa	tca	528
Gly	Thr	Lys	Asp	Lys	Gly	Ala	Lys	Glu	Leu	Glu	Glu	Leu	Rhe	Lys	Ser	
					165		170						175			

5ukAI 1
 cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat tca gtt 576
 Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val
 180 185 190

aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 624
 Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
 195 200 205

<210> 50
 <211> 206
 <212> PRT
 <213> Borrelia afzelii

<400> 50
 Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile
 1 5 10 15
 Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu
 20 25 30
 Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp
 35 40 45
 Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser
 50 55 60
 Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp
 65 70 75 80
 Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly
 85 90 95
 Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn
 100 105 110
 Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln
 115 120 125
 Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln
 130 135 140
 Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly
 145 150 155 160
 Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu
 165 170 175
 Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys
 180 185 190
 Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 195 200 205

<210> 51
 <211> 1680
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1680)

<400> 51
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15

subA1
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
 180 185 190

atg ggt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct 624
 Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
 195 200 205

gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa 672
 Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 210 215 220

att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act 720
 Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
 225 230 235 240

ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa 768
 Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
 245 250 255

Sub R1

ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser 260 265 270	816
ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu 275 280 285	864
agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala 290 295 300	912
aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala 305 310 315 320	960
gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile 325 330 335	1008
tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp 340 345 350	1056
tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu 355 360 365	1104
act aat tca gtt aaa gaa ctt ggt cac cgt aat aat tca ggt ggg gat Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp 370 375 380	1152
tct gca tct act aat cct gat gag tct gca aaa gga cct aat ctt acc Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr 385 390 395 400	1200
gta ata agc aaa aaa att aca gat tct aat gca ttt tta ctg gct gtg Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val 405 410 415	1248
aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt tct aaa gct Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala 420 425 430	1296
att ggt aaa aaa ata aaa aat gat ggt act tta gat aac gaa gca aat Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn 435 440 445	1344
cga aac gaa tca ttg ata gca gga gct tat gaa ata tca aaa cta ata Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile 450 455 460	1392
aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag aaa aaa att Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile 465 470 475 480	1440

SubP1
 aaa gag gct aag gat tgt tcc caa aaa ttt act act aag cta aaa gat 1488
 Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp
 485 490 495
 agt cat gca gag ctt ggt ata caa agc gtt cag gat gat aat gca aaa 1536
 Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys
 500 505 510
 aaa gct att tta aaa aca cat gga act aaa gac aag ggt gct aaa gaa 1584
 Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu
 515 520 525
 ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa 1632
 Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln
 530 535 540
 gca gca tta act aat tca gtt aaa gag ctt aca aat cct gtt gtg gca 1680
 Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala
 545 550 555 560

<210> 52
 <211> 560
 <212> PRT
 <213> ospC Chimera
 <400> 52
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
 180 185 190
 Met Gly Ser Asn Ser Gly Lys Gly Asp Ser Ala Ser Thr Asn Pro
 195 200 205
 Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 210 215 220
 Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
 225 230 235 240

SubAI
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 Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
 245 250 255
 Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
 260 265 270
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
 275 280 285
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
 290 295 300
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
 305 310 315 320
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
 325 330 335
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
 340 345 350
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
 355 360 365
 Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp
 370 375 380
 Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr
 385 390 395 400
 Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val
 405 410 415
 Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala
 420 425 430
 Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn
 435 440 445
 Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile
 450 455 460
 Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile
 465 470 475 480
 Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp
 485 490 495
 Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys
 500 505 510
 Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu
 515 520 525
 Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln
 530 535 540
 Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala
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 <211> 1137
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 <213> ospC Chimera

<220>
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 1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

SubAI

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 35 40 45	144
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile 50 55 60	192
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 65 70 75 80	240
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser 85 90 95	288
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys 100 105 110	336
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln 115 120 125	384
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu 130 135 140	432
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys 145 150 155 160	480
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu 165 170 175	528
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn 180 185 190	576
tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly 195 200 205	624
cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe 210 215 220	672
tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu 225 230 235 240	720
ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp 245 250 255	768

Sakai

aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile 260 265 270	816
tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu 275 280 285	864
aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr 290 295 300	912
aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp 305 310 315 320	960
gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag Asp Asn Ala Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys 325 330 335	1008
ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser 340 345 350	1056
aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn 355 360 365	1104
cct gtt gtg gca gaa agt cca aaa aaa cct taa Pro Val Val Ala Glu Ser Pro Lys Lys Pro *	1137
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SubAI
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
 180 185 190
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
 195 200 205
 Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 210 215 220
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
 225 230 235 240
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
 245 250 255
 Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
 260 265 270
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
 275 280 285
 Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
 290 295 300
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
 305 310 315 320
 Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
 325 330 335
 Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
 340 345 350
 Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
 355 360 365
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 370 375

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 <213> ospC Chimera

<220>
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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80

Sub A1

ttg tta ccg gga gct tat gca ata tca acc cta ata aaa caa aaa tta Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu 85 90 95	288
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 100 105 110	336
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp 115 120 125	384
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu 130 135 140	432
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 145 150 155 160	480
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys 180 185 190	576
aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat Lys Pro Phe His Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn 195 200 205	624
cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys 210 215 220	672
att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala 225 230 235 240	720
ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile 245 250 255	768
aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 260 265 270	816
ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser 275 280 285	864
gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp 290 295 300	912

60/102

Sub A1

tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt	960
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu	
305 310 315 320	
ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa	1008
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys	
325 330 335	
aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt	1056
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe	
340 345 350	
aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat	1104
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn	
355 360 365	
tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa	1152
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys	
370 375 380	
cct taa	1158
Pro *	
385	

<210> 56
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<212> PRT
<213> ospC Chimera

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20 25 30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
35 40 45
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
85 90 95
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
100 105 110
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
115 120 125
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
130 135 140
Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
145 150 155 160
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
165 170 175
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys
180 185 190
Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro
195 200 205
Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile
210 215 220

Sub-AI

Thr	Asp	Ser	Asn	Ala	Phe	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu
225					230				235						240
Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ser	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys
				245				250							255
Asn	Asp	Gly	Thr	Leu	Asp	Asn	Glu	Ala	Asn	Arg	Asn	Glu	Ser	Leu	Ile
			260				265			270					
Ala	Gly	Ala	Tyr	Glu	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Ser	Val
			275				280			285					
Leu	Asn	Ser	Glu	Glu	Leu	Lys	Lys	Ile	Lys	Glu	Ala	Lys	Asp	Cys	
			290			295			300						
Ser	Gln	Lys	Phe	Thr	Thr	Lys	Leu	Lys	Asp	Ser	His	Ala	Glu	Leu	Gly
			305		310				315						320
Ile	Gln	Ser	Val	Gln	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr
			325				330								335
His	Gly	Thr	Lys	Asp	Lys	Gly	Ala	Lys	Glu	Leu	Glu	Glu	Leu	Phe	Lys
			340			345				350					
Ser	Leu	Glu	Ser	Leu	Ser	Lys	Ala	Ala	Gln	Ala	Ala	Leu	Thr	Asn	Ser
			355			360				365					
Val	Lys	Glu	Leu	Thr	Asn	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro
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<211> 1161
<212> DNA
<213> ospC Chimera

<220>
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Met	Cys	Ser	Asn	Ser	Gly	Lys	Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro
1									10						15
gct	gac	gag	tct	gcg	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agc	aaa	aaa
Ala	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys
									25						30
att	aca	gat	tct	aat	gca	ttt	gta	ctt	gct	aaa	gaa	gtt	gag	act	144
Ile	Thr	Asp	Ser	Asn	Ala	Phe	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr
									40						45
ttg	gtt	tta	tct	ata	gat	gaa	ctt	gct	aag	aaa	gct	att	ggt	caa	aaa
Leu	Val	Leu	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Gln	Lys	
									55						60
ata	gac	aat	aat	aat	ggt	tta	gct	tta	aat	cag	aat	gga	tcg		240
Ile	Asp	Asn	Asn	Asn	Gly	Leu	Ala	Ala	Leu	Asn	Asn	Gln	Asn	Gly	Ser
									70						80
ttg	tta	gca	gga	gcc	tat	gca	ata	tca	acc	cta	ata	aca	gaa	aaa	ttg
Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Thr	Glu	Lys	Leu
									85						95
agt	aaa	ttg	aaa	aat	tta	gaa	gaa	tta	aag	aca	gaa	att	gca	aag	gct
Ser	Lys	Leu	Lys	Asn	Leu	Glu	Glu	Leu	Lys	Thr	Glu	Ile	Ala	Lys	Ala
									100						110

Sub A1

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca	384
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala	
115 120 125	
gat ctt ggc aaa cag gat gct acc gat cat gca aaa gca gct att	432
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile	
130 135 140	
tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat	480
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp	
145 150 155 160	
tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta	528
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu	
165 170 175	
act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt cca	576
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro	
180 185 190	
aaa aaa cct cat atg gct aat aat tca ggt ggg gat tct gca tct act	624
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
195 200 205	
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa	672
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
210 215 220	
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag	720
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
225 230 235 240	
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa	768
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys	
245 250 255	
ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca	816
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser	
260 265 270	
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta	864
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu	
275 280 285	
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag	912
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys	
290 295 300	
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag	960
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu	
305 310 315 320	
ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta	1008
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu	
325 330 335	

Sub A1

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta	1056
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu	
340 345 350	
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act	1104
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr	
355 360 365	
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa	1152
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys	
370 375 380	
aaa cct taa	1161
Lys Pro *	
385	
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<211> 386	
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<213> ospC Chimera	
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Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr	
35 40 45	
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys	
50 55 60	
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser	
65 70 75 80	
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu	
85 90 95	
Ser Lys Leu Lys Asn Leu Glu Leu Lys Thr Glu Ile Ala Lys Ala	
100 105 110	
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala	
115 120 125	
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile	
130 135 140	
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp	
145 150 155 160	
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu	
165 170 175	
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro	
180 185 190	
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
195 200 205	
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
210 215 220	
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
225 230 235 240	
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys	
245 250 255	
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser	
260 265 270	
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu	
275 280 285	

Sub-A1

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Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys
290           295           300
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
305           310           315           320
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
325           330           335
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
340           345           350
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
355           360           365
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
370           375           380
Lys Pro
385

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<210> 59
<211> 1197
<212> DNA
<213> ospC Chimera

<220>
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<222> (1)...(1197)

<400> 59	48
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys	
1 5 10 15	
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65 70 75 80	
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288
Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp	
85 90 95	
acc gaa tat aat cac aat gga tca ttg tta ggc gga gct tat gca ata	336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100 105 110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115 120 125	

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205

cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat 672
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
 210 215 220

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat 720
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 225 230 235 240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc 768
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 245 250 255

gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct 816
 Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala
 260 265 270

aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag 864
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu
 275 280 285

gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac 912
 Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn
 290 295 300

tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag 960
 Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys
 305 310 315 320

gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa 1008
 Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys
 325 330 335

tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat 1056
 Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
 340 345 350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc 1104
 Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
 355 360 365

Sub A1

S1 S2 S3 S4 S5 S6 S7 S8 S9 S10

Sub A1

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
 370 375 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197
 Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

<210> 60
 <211> 398
 <212> PRT
 <213> ospC Chimera

<400> 60
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys Ala 15
 1 5 10 15
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp 30
 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn 45
 35 40 45
 Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu Leu 60
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala 80
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp Thr 95
 85 90 95
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser 110
 100 105 110
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys 125
 115 120 125
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys 140
 130 135 140
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala 160
 145 150 155 160
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly 175
 165 170 175
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys 190
 180 185 190
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro 205
 195 200 205
 Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp Gly 220
 210 215 220
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu 240
 225 230 235 240
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala 255
 245 250 255
 Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys 270
 260 265 270
 Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala 285
 275 280 285
 Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu 300
 290 295 300
 Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala 320
 305 310 315 320
 Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu 335
 325 330 335

67/102

<210> 61
<211> 1196
<212> DNA
<213> ospC Chimera

<220>
<221> CDS

Sub A1
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gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat	672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp	
210 215 220	
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat	720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
225 230 240	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg	768
Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
245 250 255	
gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct	816
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala	
260 265 270	
act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc	864
Thr Lys Ala Ile Gly Lys Ile Gln Gln Asn Gly Gly Leu Ala Val	
275 280 285	
gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca	912
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
290 295 300	
aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta	960
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu	
305 310 320	
aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa	1008
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys	
325 330 335	
aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat	1056
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp	
340 345 350	
gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag	1104
Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys	
355 360 365	
ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca	1152
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala	
370 375 380	

Sab A1

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt ac	1196
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu	
385	390
	395

<210> 62
<211> 397
<212> PRT
<213> ospC Chimera

<400> 62

Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Ile Gly Cys Ala			
1	5	10	15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp			
20	25	30	
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn			
35	40	45	
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu			
50	55	60	
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala			
65	70	75	80
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr			
85	90	95	
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser			
100	105	110	
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys			
115	120	125	
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys			
130	135	140	
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala			
145	150	155	160
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly			
165	170	175	
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys			
180	185	190	
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro			
195	200	205	
Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp Gly			
210	215	220	
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu			
225	230	235	240
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala			
245	250	255	
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr			
260	265	270	
Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu			
275	280	285	
Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys			
290	295	300	
Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys			
305	310	315	320
Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys			
325	330	335	
Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu			
340	345	350	
Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly			
355	360	365	

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Suh AI
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys
370 375 380
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385 390 395

<210> 63
<211> 1185
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1185)

<400> 63
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu
65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
Ala Lys Ala Ile Gly Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175

SubhAI

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	576
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	624
195 200 205	
agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser	672
210 215 220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	720
225 230 235 240	
agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	768
245 250 255	
gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly	816
260 265 270	
aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn	864
275 280 285	
gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys	912
290 295 300	
aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu	960
305 310 315 320	
aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu	1008
325 330 335	
cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys	1056
340 345 350	
gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu	1104
355 360 365	
gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu	1152
370 375 380	
atg ctt act aat tca gtt aaa gag ctt aca agc Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser	1185
385 390 395	

Sub A1

<211> 394
<212> PRT
<213> ospC Chimera

<400> 64
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
1 5 10 15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
65 70 75 80
Lys Ala Ile Gly Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
85 90 95
Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
100 105 110
Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
115 120 125
Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
130 135 140
Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
145 150 155 160
Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
165 170 175
Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
180 185 190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195 200 205
Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
210 215 220
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
225 230 235 240
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
245 250 255
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys
260 265 270
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly
275 280 285
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys
290 295 300
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys
305 310 315 320
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His
325 330 335
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
340 345 350
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
355 360 365
Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
370 375 380
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
385 390

<210> 65
<211> 1184

Sub A1

<212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1184)

<400> 65	atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt	48	
	Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys		
1	5	10	
		15	
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa	96		
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144		
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192		
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240		
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu			
65	70	75	80
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288		
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn			
85	90	95	
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336		
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser			
100	105	110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384		
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu			
115	120	125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432		
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr			
130	135	140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480		
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp			
145	150	155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528		
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp			
165	170	175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576		
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu			
180	185	190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624		
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Deu Thr			
195	200	205	

Sub A1

agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser	672
210 215 220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	720
225 230 235 240	
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	768
245 250 255	
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile	816
260 265 270	
ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His	864
275 280 285	
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr	912
290 295 300	
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile	960
305 310 315 320	
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly	1008
325 330 335	
gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys	1056
340 345 350	
aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu	1104
355 360 365	
ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys	1152
370 375 380	
gag atg ctt gct aat tca gtt aaa gag ctt ac Glu Met Leu Ala Asn Ser Val Lys Glu Leu	1184
385 390	
<210> 66	
<211> 393	
<212> PRT	
<213> ospC Chimera	
<400> 66	
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala	
1 5 10 15	

Sub A1
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
 65 70 75 80
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
 85 90 95
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
 100 105 110
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
 130 135 140
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
 145 150 155 160
 Asn Ala Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
 165 170 175
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
 210 215 220
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
 225 230 235 240
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile
 245 250 255
 Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
 260 265 270
 Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn
 275 280 285
 Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln
 290 295 300
 Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu
 305 310 315 320
 Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu
 325 330 335
 His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys
 340 345 350
 Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
 355 360 365
 Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu
 370 375 380
 Met Leu Ala Asn Ser Val Lys Glu Leu
 385 390

<210> 67
 <211> 1184
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1184)

Sub A1

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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys		
1 5 10 15		
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa		96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys		
20 25 30		
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct		144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro		
35 40 45		
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta		192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu		
50 55 60		
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt		240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu		
65 70 75 80		
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat		288
Ala Lys Ala Ile Gly Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn		
85 90 95		
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca		336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser		
100 105 110		
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta		384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu		
115 120 125		
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act		432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr		
130 135 140		
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat		480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp		
145 150 155 160		
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat		528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp		
165 170 175		
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta		576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu		
180 185 190		
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca		624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr		
195 200 205		
agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct		672
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser		
210 215 220		

Sub AI

aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile 225 230 235 240	720
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu 245 250 255	768
gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile 260 265 270	816
ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn 275 280 285	864
aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu 290 295 300	912
aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr 305 310 315 320	960
gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His 325 330 335	1008
gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala 340 345 350	1056
att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu 355 360 365	1104
aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr 370 375 380	1152
tta aaa aat gct gtt aaa gag ctt aca agt cc Leu Lys Asn Ala Val Lys Glu Leu Thr Ser 385 390	1184

<210> 68
<211> 393
<212> PRT
<213> ospC Chimera

<400> 68
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Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60

SubA1

SubB2

Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
 65 70 75 80
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
 85 90 95
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
 100 105 110
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
 130 135 140
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
 145 150 155 160
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
 165 170 175
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr
 210 215 220
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
 225 230 235 240
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
 245 250 255
 Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
 260 265 270
 Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr
 275 280 285
 Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys
 290 295 300
 Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala
 305 310 315 320
 Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala
 325 330 335
 Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile
 340 345 350
 Leu Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys
 355 360 365
 Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu
 370 375 380
 Lys Asn Ala Val Lys Glu Leu Thr Ser
 385 390

<210> 69
<211> 1209
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1209)

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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

Sub A1

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 20 25 30	96
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 35 40 45	144
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 50 55 60	192
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu 65 70 75 80	240
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat Ala Lys Ala Ile Gly Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn 85 90 95	288
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser 100 105 110	336
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu 115 120 125	384
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr 130 135 140	432
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp 145 150 155 160	480
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat Glu Asn Ala Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp 165 170 175	528
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta Lys Gly Val Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu 180 185 190	576
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr 195 200 205	624
agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr 210 215 220	672
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys 225 230 235 240	720
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu 245 250 255	768

Sub A1

gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys 260 265 270	816
ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser 275 280 285	864
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu 290 295 300	912
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys 305 310 315 320	960
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu 325 330 335	1008
ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu 340 345 350	1056
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu 355 360 365	1104
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr 370 375 380	1152
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys 385 390 395 400	1200
aaa cct taa Lys Pro *	1209

<210> 70
<211> 401
<212> PRT
<213> ospC Chimera

<400> 70
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Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
65 70 75 80

Sub A1

Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
 85 90 95
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
 100 105 110
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
 130 135 140
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
 145 150 155 160
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
 165 170 175
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn
 210 215 220
 Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys
 225 230 235 240
 Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala
 245 250 255
 Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile
 260 265 270
 Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 275 280 285
 Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
 290 295 300
 Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys Asp
 305 310 315 320
 Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
 325 330 335
 Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
 340 345 350
 Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Leu Phe
 355 360 365
 Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
 370 375 380
 Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
 385 390 395 400
 Pro

<210> 71
 <211> 1179
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1179)

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

82/102

Sub A1

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 20 25 30	96
gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 35 40 45	144
aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val 50 55 60	192
ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu 65 70 75 80	240
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala 85 90 95	288
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser 100 105 110	336
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys 115 120 125	384
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys 130 135 140	432
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp 145 150 155 160	480
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly 165 170 175	528
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys 180 185 190	576
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro 195 200 205	624
att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn 210 215 220	672
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys 225 230 235 240	720
aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu 245 250 255	768

SubAI

act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa	816
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys	
260 265 270	
ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca	864
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser	
275 280 285	
tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata	912
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile	
290 295 300	
agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct	960
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala	
305 310 315 320	
aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca	1008
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr	
325 330 335	
gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att	1056
Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile	
340 345 350	
tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag	1104
Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys	
355 360 365	
tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt	1152
Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu	
370 375 380	
act aat tca gtt aaa gag ctt aca agc	1179
Thr Asn Ser Val Lys Glu Leu Thr Ser	
385 390	
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<211> 392	
<212> PRT	
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Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp	
20 25 30	
Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
35 40 45	
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
50 55 60	
Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala	
65 70 75 80	
Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn	
85 90 95	
Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp	
100 105 110	

SukhAI 1

Leu	Ile	Ala	Glu	Lys	Leu	Asn	Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys	Glu
115					120						125				
Lys	Ile	Asp	Thr	Ala	Lys	Gln	Cys	Ser	Thr	Glu	Phe	Thr	Asn	Lys	Leu
130					135						140				
Lys	Ser	Glu	His	Ala	Val	Leu	Gly	Leu	Asp	Asn	Leu	Thr	Asp	Asp	Asn
145					150					155					160
Ala	Gln	Arg	Ala	Ile	Leu	Lys	Lys	His	Ala	Asn	Lys	Asp	Lys	Gly	Ala
					165					170					175
Ala	Glu	Leu	Glu	Dys	Leu	Phe	Lys	Ala	Val	Glu	Asn	Leu	Ser	Lys	Ala
					180					185					190
Ala	Gln	Asp	Thr	Ile	Lys	Asn	Ala	Val	Lys	Glu	Leu	Thr	Ser	Pro	Ile
					195					200					205
Val	His	Gly	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser
					210					215					220
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys
					225					230					240
Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr
					245					250					255
Leu	Leu	Thr	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile
					260					265					270
Lys	Asn	Asp	Val	Ser	Leu	Asp	Asn	Glu	Ala	Asp	His	Asn	Gly	Ser	Leu
					275					280					285
Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn	Leu	Ile	Thr	Lys	Lys	Ile	Ser
					290					295					300
Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys	Ala	Lys
					305					310					320
Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu	Lys	Gly	Glu	His	Thr	Asp
					325					330					335
Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu
					340					345					350
Lys	Thr	Asn	Asn	Asp	Lys	Thr	Lys	Gly	Ala	Asp	Glu	Leu	Glu	Lys	Leu
					355					360					365
Phe	Glu	Ser	Val	Lys	Asn	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Thr
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Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser								
					385					390					

<210> 73

<211> 1178

<212> DNA

<213> ospC Chimera

<220>

<221> CDS

<222> (1)...(1178)

<400> 73

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1										10					15

gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	gga	aaa
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys
															96
20										25					30

gat	ggg	aat	gca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	cct
Asp	Gly	Asn	Ala	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro
															144
35										40					45

Sub A1

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val	
50 55 60	
ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt	240
Leu Ala Val Lys Glu Val Glu Thr Leu Ala Ser Ile Asp Glu Leu	
65 70 75 80	
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288
Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala	
85 90 95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	
100 105 110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	
115 120 125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	
130 135 140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asn Asn Leu Thr Asp Asp	
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	
att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat	672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn	
210 215 220	
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu	
245 250 255	
act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa	816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys	
260 265 270	

SubfA1

aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly 275 280 285	864
aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys 290 295 300	912
tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn 305 310 315 320	960
gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His 325 330 335	1008
gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala 340 345 350	1056
att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu 355 360 365	1104
aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met 370 375 380	1152
ctt gct aat tca gtt aaa gag ctt ac Leu Ala Asn Ser Val Lys Glu Leu 385 390	1178
<210> 74 <211> 391 <212> PRT <213> ospC Chimera	
<400> 74 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys Ala 1 5 10 15 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp 20 25 30 Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn 35 40 45 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu 50 55 60 Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala 65 70 75 80 Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn 85 90 95 Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp 100 105 110 Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu 115 120 125 Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu 130 135 140 Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn 145 150 155 160	

Sub A1

Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala
 165 170 175
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala
 180 185 190
 Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile
 195 200 205
 Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 210 215 220
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 225 230 235 240
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr
 245 250 255
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 260 265 270
 Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr
 275 280 285
 Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu
 290 295 300
 Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala
 305 310 315 320
 Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala
 325 330 335
 Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile
 340 345 350
 Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys
 355 360 365
 Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu
 370 375 380
 Ala Asn Ser Val Lys Glu Leu
 385 390

<210> 75
 <211> 1178
 <212> DNA
 <213> ospC Chimera

 <220>
 <221> CDS
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60

Sub A1

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu 65 70 75 80	240
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala 85 90 95	288
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser 100 105 110	336
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys 115 120 125	384
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys 130 135 140	432
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp 145 150 155 160	480
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly 165 170 175	528
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys 180 185 190	576
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro 195 200 205	624
att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn 210 215 220	672
tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys 225 230 235 240	720
aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu 245 250 255	768
acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys 260 265 270	816
aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser 275 280 285	864
ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu 290 295 300	912

Sust A1

aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag 960
 Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
 305 310 315 320

caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg 1008
 Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
 325 330 335

ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta 1056
 Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
 340 345 350

aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta 1104
 Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
 355 360 365

ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa 1152
 Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
 370 375 380

aat gct gtt aaa gag ctt aca agt cc 1178
 Asn Ala Val Lys Glu Leu Thr Ser
 385 390

<210> 76
<211> 391
<212> PRT
<213> ospC Chimera

<400> 76
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys Ala 15
 1 5 10 15
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp 30
 20 25 30
 Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn 45
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu 60
 50 55 60
 Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala 80
 65 70 75 80
 Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn 95
 85 90 95
 Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp 110
 100 105 110
 Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu 125
 115 120 125
 Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu 140
 130 135 140
 Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn 160
 145 150 155 160
 Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala 175
 165 170 175
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala 190
 180 185 190
 Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile 205
 195 200 205

Sub A1

Val	His	Gly	Asn	Asn	Ser	Arg	Lys	Asp	Gly	Asn	Ala	Ser	Thr	Asn	Ser
210						215					220				
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys
225					230					235				240	
Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr
				245				250				255			
Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys
				260				265				270			
Ile	Gly	Asn	Asn	Gly	Leu	Glu	Ala	Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu
				275				280				285			
Leu	Ser	Gly	Ala	Tyr	Ala	Ile	Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn
				290				295				300			
Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln
305					310				315				320		
Cys	Ser	Thr	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Glu	His	Ala	Val	Leu
				325				330				335			
Gly	Leu	Asp	Asn	Leu	Thr	Asp	Asp	Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys
				340				345				350			
Lys	His	Ala	Asn	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe
				355				360				365			
Lys	Ala	Val	Glu	Asn	Leu	Ser	Lys	Ala	Ala	Gln	Asp	Thr	Leu	Lys	Asn
				370				375				380			
Ala	Val	Lys	Glu	Leu	Thr	Ser									
				385				390							

<210> 77

<211> 1230

<212> DNA

<213> ospC Chimera

<220>

<221> CDS

<222> (1)...(1230)

<400> 77

atg	aga	tta	tta	ata	gga	ttt	gtc	tta	gct	tta	ata	gga	tgt		48
Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys
1					5				10				15		

gca	caa	aaa	ggg	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	ggg	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	
								20		25			30			

gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	aaa	ggg	cct		144
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	
								35		40		45				

aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	acg	gat	tct	aat	gcg	gtt	tta	192
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	
								50		55		60				

ctt	gct	gtg	aaa	gag	gtt	gaa	gcf	ttg	ctg	tca	tct	ata	gat	gaa	att	240
Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	
								65		70		75		80		

gct	gct	aaa	gct	att	ggt	aaa	aaa	ata	cac	caa	aat	aat	ggt	ttg	gat	288
Ala	Ala	Lys	Ala	Ile	Gly	Lys	Ile	His	Gln	Asn	Asn	Gly	Leu	Asp		
								85		90		95				

,ub R1

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 100	105	110	336
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 115	120	125	384
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 130	135	140	432
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 145	150	155	480
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 165	170	175	528
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 180	185	190	576
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 195	200	205	624
cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser 210	215	220	672
ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro 225	230	235	720
aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta Asn Leu Thr Val Ile Ser Lys Ile Thr Asp Ser Asn Ala Phe Leu 245	250	255	768
ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu 260	265	270	816
tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn 275	280	285	864
gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser 290	295	300	912
aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys 305	310	315	960

Salt A1

aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys 325 330 335	1008
cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp 340 345 350	1056
aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly 355 360 365	1104
gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys 370 375 380	1152
gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro 385 390 395 400	1200
gtt gtg gca gaa agt cca aaa aaa cct taa Val Val Ala Glu Ser Pro Lys Lys Pro * 405	1230

<210> 78
<211> 408
<212> PRT
<213> ospC Chimera

<400> 78
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys Ala
1 5 10 15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
65 70 75 80
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
85 90 95
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
100 105 110
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
115 120 125
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
130 135 140
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
145 150 155 160
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
165 170 175
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
180 185 190
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
195 200 205
Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser Gly
210 215 220

Sub A1

Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn
225					230				235					240	
Leu	Thr	Val	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	Leu	Leu
			245					250					255		
Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ser
		260					265				270				
Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Thr	Leu	Asp	Asn	Glu
		275				280				285					
Ala	Asn	Arg	Asn	Glu	Ser	Leu	Ile	Ala	Gly	Ala	Tyr	Glu	Ile	Ser	Lys
		290			295				300						
Leu	Ile	Thr	Gln	Lys	Leu	Ser	Val	Leu	Asn	Ser	Glu	Glu	Leu	Lys	Lys
		305			310			315				320			
Lys	Ile	Lys	Glu	Ala	Lys	Asp	Cys	Ser	Gln	Lys	Phe	Thr	Thr	Lys	Leu
		325				330				335					
Lys	Asp	Ser	His	Ala	Glu	Leu	Gly	Ile	Gln	Ser	Val	Gln	Asp	Asp	Asn
		340				345				350					
Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	His	Gly	Thr	Lys	Asp	Lys	Gly	Ala
		355				360				365					
Lys	Glu	Leu	Glu	Glu	Leu	Phe	Lys	Ser	Leu	Glu	Ser	Leu	Ser	Lys	Ala
		370				375				380					
Ala	Gln	Ala	Ala	Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Asn	Pro	Val
		385				390			395				400		
Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro								
					405										

<210> 79
<211> 1209
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1209)

<400> 79	48
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys	
1 5 10 15	
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65 70 75 80	
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp	
85 90 95	

SukrAI 1

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 100 105 110	336
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 115 120 125	384
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 130 135 140	432
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 145 150 155 160	480
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 165 170 175	528
ggg gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 180 185 190	576
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 195 200 205	624
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser 210 215 220	672
ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys 225 230 235 240	720
ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala 245 250 255	768
gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp 260 265 270	816
gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu 275 280 285	864
gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu 290 295 300	912
att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly 305 310 315 320	960
gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt	1008

Sub A1

Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe 325 330 335	
act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val 340 345 350	1056
act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys 355 360 365	1104
act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn 370 375 380	1152
ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu 385 390 395 400	1200
aca agc taa Thr Ser *	1209

<210> 80
<211> 401
<212> PRT
<213> ospC Chimera

<400> 80	
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1 5 10 15	
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp	
20 25 30	
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
35 40 45	
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu	
50 55 60	
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala	
65 70 75 80	
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr	
85 90 95	
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser	
100 105 110	
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys	
115 120 125	
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys	
130 135 140	
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala	
145 150 155 160	
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly	
165 170 175	
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys	
180 185 190	
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro	
195 200 205	
Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser Gly	
210 215 220	

96/102

Sub A' 1

Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
225 230 235 240
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
245 250 255
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu
260 265 270
Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp
275 280 285
Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile
290 295 300
Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu
305 310 315 320
Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
325 330 335
Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr
340 345 350
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr
355 360 365
Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu
370 375 380
Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
385 390 395 400
Ser

<210> 81
<211> 1205
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1205)

<400> 81

atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95

SuAI

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100 105 110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115 120 125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa dac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca	672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser	
210 215 220	
gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa	720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys	
225 230 235 240	
ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca	768
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala	
245 250 255	
gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat	816
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp	
260 265 270	
gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt	864
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly	
275 280 285	
tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat	912
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr	
290 295 300	
aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca	960
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser	
305 310 315 320	

Sub A1

gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp 325 330 335	1008
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn 340 345 350	1056
gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala 355 360 365	1104
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu 370 375 380	1152
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu 385 390 395 400	1200
ctt ac Leu	1205

<210> 82
<211> 400
<212> PRT
<213> ospC Chimera

<400> 82
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
1 5 10 15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
65 70 75 80
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
85 90 95
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
100 105 110
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
115 120 125
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
130 135 140
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
145 150 155 160
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
165 170 175
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
180 185 190
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
195 200 205
Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser Gly
210 215 220

99/102

Sub A1

Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
225 230 235 240
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
245 250 255
Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu
260 265 270
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu
275 280 285
Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr
290 295 300
Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu
305 310 315 320
Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe
325 330 335
Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val
340 345 350
Thr Asp Glu Asn Ala Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys
355 360 365
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
370 375 380
Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385 390 395 400

<210> 83
<211> 1236
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1236)

<400> 83
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
gca caa aaa ggt gct gag tca att gga tcc tgt agt aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys
20 25 30
ggg ggg gat tct gca tct act aat cct gct gac gag tct gcg aaa ggg 144
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly
35 40 45
cct aat ctt aca gaa ata agc aaa aaa att aca gat tct aat gca ttt 192
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
50 55 60
gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa 240
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu
65 70 75 80
ctt gct aag aaa gct att ggt caa aaa ata gac aat aat aat ggt tta 288
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu
85 90 95

100/102

Sub A1

gct gct tta aat aat cag aat gga tcg ttg tta gca gga gcc tat gca Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala	336
100 105 110	
ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu	384
115 120 125	
gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe	432
130 135 140	
act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala	480
145 150 155 160	
acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr	528
165 170 175	
gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly	576
180 185 190	
ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu	624
195 200 205	
aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn	672
210 215 220	
aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys	720
225 230 235 240	
gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala	768
245 250 255	
ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp	816
260 265 270	
gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu	864
275 280 285	
gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu	912
290 295 300	
ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu	960
305 310 315 320	
tta aag aaa aaa att aaa gag gct aag gat tgg ttc caa aaa ttt act Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr	1008
325 330 335	

Sub A1

act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag	1056
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln	
340	345
350	
gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac	1104
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp	
355	360
365	
aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg	1152
Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu	
370	375
380	
tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca	1200
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr	
385	390
395	400
aat cct gtt gtg gca gaa agt cca aaa aaa cct taa	1236
Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *	
405	410

<210> 84
<211> 410
<212> PRT
<213> ospC Chimera

<400> 84

Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala			
1	5	10	15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys Gly			
20	25	30	
Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly Pro			
35	40	45	
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Val			
50	55	60	
Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu Leu			
65	70	75	80
Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu Ala			
85	90	95	
Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile			
100	105	110	
Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu Glu			
115	120	125	
Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr			
130	135	140	
Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala Thr			
145	150	155	160
Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr Asp			
165	170	175	
Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly Leu			
180	185	190	
Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu Thr			
195	200	205	
Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn Asn			
210	215	220	
Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly			
225	230	235	240

SubP1 1

Pro	Asn	Leu	Thr	Val	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe
245							250							255	
Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu
260						265							270		
Leu	Ser	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Thr	Leu	Asp
275					280						285				
Asn	Glu	Ala	Asn	Arg	Asn	Glu	Ser	Leu	Ile	Ala	Gly	Ala	Tyr	Glu	Ile
290						295					300				
Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Ser	Val	Leu	Asn	Ser	Glu	Glu	Leu
305						310				315				320	
Lys	Lys	Lys	Ile	Lys	Glu	Ala	Lys	Asp	Cys	Ser	Gln	Lys	Phe	Thr	Thr
325							330						335		
Lys	Leu	Lys	Asp	Ser	His	Ala	Glu	Leu	Gly	Ile	Gln	Ser	Val	Gln	Asp
340							345						350		
Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	His	Gly	Thr	Lys	Asp	Lys
355							360						365		
Gly	Ala	Lys	Glu	Leu	Glu	Glu	Leu	Phe	Lys	Ser	Leu	Glu	Ser	Leu	Ser
370						375					380				
Lys	Ala	Ala	Gln	Ala	Ala	Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Asn
385						390					395				400
Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro						
				405					410						